

RAW SEQUENCE LISTING

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Application Serial Number: 10/562,778
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PATENT APPLICATION: US/10/562,778

DATE: 08/24/2006

TIME: 15:01:14

Input Set : A:\Sequence Listing.ST25.txt

Output Set: N:\CRF4\08242006\J562778.raw

3 <110> APPLICANT: Chai, Zhonglin
 4 Cooper, Mark Emmanuel
 5 Cao, Zemin
 7 <120> TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING DISORDERS OF THE
 8 EXTRACELLULAR MATRIX
 10 <130> FILE REFERENCE: 002354/000370
 12 <140> CURRENT APPLICATION NUMBER: 10/562,778
 13 <141> CURRENT FILING DATE: 2005-12-29
 15 <150> PRIOR APPLICATION NUMBER: AU2003903363
 16 <151> PRIOR FILING DATE: 2003-07-01
 18 <150> PRIOR APPLICATION NUMBER: PCT/AU2004/000873
 19 <151> PRIOR FILING DATE: 2004-06-30
 21 <160> NUMBER OF SEQ ID NOS: 2
 23 <170> SOFTWARE: PatentIn version 3.3
 25 <210> SEQ ID NO: 1
 26 <211> LENGTH: 2867
 27 <212> TYPE: DNA
 28 <213> ORGANISM: Homo sapiens
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 35 cggtcgccat ggaccggccaa gatgaggggc ctccggccaa gaccggccgc ctgagcagct 180
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 41 tggccgatat gaggggggtg ggactgggccc cgcgcgtgcc cccggccgcct ccctatgtca 360
 43 ttctcgagga gggggggatc cgcgcataact tcacgctcg tgctgagtgt cccggctggg 420
 45 attctaccat cgagtcgggg tatggggagg ccgcggccgc cacggagagc ctggaaagcac 480
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 55 ggaaggtgaa gagggaaagc agagagagaa atgcccggagag gatggagagc atcctgcagg 780
 57 cactggagga tattcagctg gatctggagg cagttaacat caaggcagggc aaaggccttcc 840
 59 tgcgtctcaa ggcgaagttc atccagatgc gaagaccctt cctggagcgc agagaccta 900
 61 tcatccagca tatcccaggc ttctgggtca aagcattcct caaccacccc agaatttcaa 960
 63 tttgtatcaa cgcacgtgat gaagacattt tccgctactt gaccaatctg caggtacagg 1020
 65 attcagaca tatctccatg ggctacaaaa tgaagctgta cttccagact aaccctact 1080
 67 tcacaaacat ggtgattgtc aaggagttcc agcgcacccg ctcaggccgg ctgggtctc 1140
 69 actcaacccc aatccgctgg caccggggcc aggaacccc ggcggcgtcgt cacggaaacc 1200
 71 aggatgcgag ccacagctt ttcaagctgg tctcaaacca tagcctccca gaggctgaca 1260
 73 ggattgctga gattatcaag aatgatctgt gggtaaccc tctacgctac tacctgagag 1320
 75 aaaggggctc caggataaaag agaaaagaagc aagaatgaa gaaacgtaaa accaggggca 1380
 77 gatgtgaggt ggtgatcatg gaagacgccc ctgactatta tgcagtggaa gacattttca 1440

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83	acagcgagaa	tcctgaccac	aatgaggtcc	ccaacaacga	gaccactgat	aacaacgaga	1620									
85	gcgcgtatga	ccacgaaacc	actgacaaca	atgagagtgc	agatgacaac	aacgagaatc	1680									
87	ctgaagacaa	taacaagaac	actgtatgaca	acgaagagaa	ccctaacaac	aacgagaaca	1740									
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117	ggccttcgtc	acagccgcgc	agtgcctatg	gaggcgctgc	tgccaccttc	ctctcccaag	2640									
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140					20				25			30				
143	Pro	Leu	Leu	Arg	Leu	Pro	Leu	Pro	Pro	Pro	Gln	Gln	Arg	Pro	Arg	Leu
144					35				40			45				
147	Gln	Glu	Glu	Thr	Glu	Ala	Ala	Gln	Val	Leu	Ala	Asp	Met	Arg	Gly	Val
148					50				55			60				
151	Gly	Leu	Gly	Pro	Ala	Leu	Pro	Pro	Pro	Pro	Tyr	Val	Ile	Leu	Glu	
152	65					70				75			80			
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156						85				90			95			
159	Trp	Asp	Ser	Thr	Ile	Glu	Ser	Gly	Tyr	Gly	Glu	Ala	Pro	Pro	Pro	Thr
160						100			105			110				
163	Glu	Ser	Leu	Glu	Ala	Leu	Pro	Thr	Pro	Glu	Ala	Ser	Gly	Gly	Ser	Leu
164						115			120			125				
167	Glu	Ile	Asp	Phe	Gln	Val	Val	Gln	Ser	Ser	Ser	Phe	Gly	Gly	Glu	Gly
168						130			135			140				
171	Ala	Leu	Glu	Thr	Cys	Ser	Ala	Val	Gly	Trp	Ala	Pro	Gln	Arg	Leu	Val
172	145					150				155			160			

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175 Asp Pro Lys Ser Lys Glu Glu Ala Ile Ile Ile Val Glu Asp Glu Asp
176 165 170 175
179 Glu Asp Glu Arg Glu Ser Met Arg Ser Ser Arg Arg Arg Arg Arg Arg
180 180 185 190
183 Arg Arg Arg Lys Gln Arg Lys Val Lys Arg Glu Ser Arg Glu Arg Asn
184 195 200 205
187 Ala Glu Arg Met Glu Ser Ile Leu Gln Ala Leu Glu Asp Ile Gln Leu
188 210 215 220
191 Asp Leu Glu Ala Val Asn Ile Lys Ala Gly Lys Ala Phe Leu Arg Leu
192 225 230 235 240
195 Lys Arg Lys Phe Ile Gln Met Arg Arg Pro Phe Leu Glu Arg Arg Asp
196 245 250 255
199 Leu Ile Ile Gln His Ile Pro Gly Phe Trp Val Lys Ala Phe Leu Asn
200 260 265 270
203 His Pro Arg Ile Ser Ile Leu Ile Asn Arg Arg Asp Glu Asp Ile Phe
204 275 280 285
207 Arg Tyr Leu Thr Asn Leu Gln Val Gln Asp Leu Arg His Ile Ser Met
208 290 295 300
211 Gly Tyr Lys Met Lys Leu Tyr Phe Gln Thr Asn Pro Tyr Phe Thr Asn
212 305 310 315 320
215 Met Val Ile Val Lys Glu Phe Gln Arg Asn Arg Ser Gly Arg Leu Val
216 325 330 335
219 Ser His Ser Thr Pro Ile Arg Trp His Arg Gly Gln Glu Pro Gln Ala
220 340 345 350
223 Arg Arg His Gly Asn Gln Asp Ala Ser His Ser Phe Phe Ser Trp Phe
224 355 360 365
227 Ser Asn His Ser Leu Pro Glu Ala Asp Arg Ile Ala Glu Ile Ile Lys
228 370 375 380
231 Asn Asp Leu Trp Val Asn Pro Leu Arg Tyr Tyr Leu Arg Glu Arg Gly
232 385 390 395 400
235 Ser Arg Ile Lys Arg Lys Lys Gln Glu Met Lys Lys Arg Lys Thr Arg
236 405 410 415
239 Gly Arg Cys Glu Val Val Ile Met Glu Asp Ala Pro Asp Tyr Tyr Ala
240 420 425 430
243 Val Glu Asp Ile Phe Ser Glu Ile Ser Asp Ile Asp Glu Thr Ile His
244 435 440 445
247 Asp Ile Lys Ile Ser Asp Phe Met Glu Thr Thr Asp Tyr Phe Glu Thr
248 450 455 460
251 Thr Asp Asn Glu Ile Thr Asp Ile Asn Glu Asn Ile Cys Asp Ser Glu
252 465 470 475 480
255 Asn Pro Asp His Asn Glu Val Pro Asn Asn Glu Thr Thr Asp Asn Asn
256 485 490 495
259 Glu Ser Ala Asp Asp His Glu Thr Thr Asp Asn Asn Glu Ser Ala Asp
260 500 505 510
263 Asp Asn Asn Glu Asn Pro Glu Asp Asn Asn Lys Asn Thr Asp Asp Asn
264 515 520 525
267 Glu Glu Asn Pro Asn Asn Asn Glu Asn Thr Tyr Gly Asn Asn Phe Phe
268 530 535 540
271 Lys Gly Gly Phe Trp Gly Ser His Gly Asn Asn Gln Asp Ser Ser Asp

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272 545 550 555 560
275 Ser Asp Asn Glu Ala Asp Glu Ala Ser Asp Asp Glu Asp Asn Asp Gly
276 565 570 575
279 Asn Glu Gly Asp Asn Glu Gly Ser Asp Asp Asp Gly Asn Glu Gly Asp
280 580 585 590
283 Asn Glu Gly Ser Asp Asp Asp Arg Asp Ile Glu Tyr Tyr Glu Lys
284 595 600 605
287 Val Ile Glu Asp Phe Asp Lys Asp Gln Ala Asp Tyr Glu Asp Val Ile
288 610 615 620
291 Glu Ile Ile Ser Asp Glu Ser Val Glu Glu Gly Ile Glu Glu Gly
292 625 630 635 640
295 Ile Gln Gln Asp Glu Asp Ile Tyr Glu Glu Gly Asn Tyr Glu Glu
296 645 650 655
299 Gly Ser Glu Asp Val Trp Glu Glu Gly Glu Asp Ser Asp Asp Ser Asp
300 660 665 670
303 Leu Glu Asp Val Leu Gln Val Pro Asn Gly Trp Ala Asn Pro Gly Lys
304 675 680 685
307 Arg Gly Lys Thr Gly
308 690

VERIFICATION SUMMARY

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